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In the Claims:

Please amend claims 35, 39 and 40 as follows:

1. (Original) A method of controlling cancer suppression in a mammal having a cancer suppressing gene, comprising the steps of:
making a substantially duplicated genetic material corresponding to the genetic material of said gene, the substantially duplicated material selected from the group consisting of a cloned cancer suppressing gene, a modified or defective cancer suppressing gene, homologues thereof, fragments thereof, and mixtures thereof; and
interchanging said duplicated genetic material and the cancer suppressing gene of the mammal.
2. (Original) A method of claim 1, wherein before said making a substantially duplicated genetic material, determining the chromosomal location of said cancer suppressing gene of the mammal.
3. (Original) A method of claim 1, wherein after said making a substantially duplicated genetic material, detecting the presence or absence of an inactive cancer suppressing gene of a tissue sample of the mammal to determine whether or not the tissue sample cancer suppressing gene is defective or absent.
4. (Original) A method of claim 3, wherein in response to a determination that the tissue sample cancer suppressing gene is either defective or absent, replacing a cancer suppressing gene of the mammal with its clone.

5. (Original) A method of claim 3, wherein the determination of whether or not the tissue sample cancer suppressing gene is defective or absent is accomplished by measuring the amount of protein product of said cancer suppressing gene, of the tissue sample, bound by an antibody specific for said protein.

6. (Original) A method of claim 5, wherein the determination of whether or not the tissue sample cancer suppressing gene is defective or absent is accomplished by:

- (a) labeling said tissue sample with radioactive isotope;
- (b) lysing the labeled tissue;
- (c) reacting the protein product of said cancer suppressing gene with an antibody specific for said protein thereby forming a protein/antibody immunocomplex;
- (d) autoradiographing the immunocomplex obtained in step (c); and
- (e) determining the presence or absence of the protein product by comparing the autoradiogram of step (d) with the autoradiogram of the standard protein product.

7. (Original) The method of claim 5, wherein the determination of whether or not the tissue sample cancer suppressing gene is defective or absent is accomplished by enzyme immunoassay techniques.

8. (Original) The method of claim 5, wherein the determination of whether or not the tissue sample cancer suppressing gene is defective or absent is accomplished by immunocytochemistry methods.

9. (Original) The method of claim 5, wherein the cancer suppressing gene is the RB gene and the protein product is ppRB¹¹⁰.

10. (Original) The method of claim 1, wherein said cancer suppressing gene is replaced with substantially duplicated material selected from the group consisting of said cloned cancer suppressing gene, homologues thereof, fragments thereof, and mixtures thereof, for therapeutic purposes.

11. (Original) The method of claim 1, wherein said cancer suppressing gene is replaced with substantially duplicated material selected from the group consisting of said defective cancer suppressing gene, homologues thereof, fragments thereof, and mixtures thereof, for facilitating the testing of the carcinogenicity of environmental influences.

12. (Original) The method of claim 2, wherein the location of said cancer suppressing gene is determined by chromosome walking.

13. (Original) The method of claim 2, wherein the location of said cancer suppressing gene is determined through organic markers.

14. (Original) A method of claim 2, wherein:
said chromosomal location of said cancer suppressing gene is determined by testing genes of a chromosome for phenotypic expression;
determining one of the genes of said chromosome to be a marker gene; and
using chromosomal walking techniques to locate a cancer suppressing gene.

15. (Original) An animal genetically altered so as to have the allele of at least one cancer suppressing gene selected from the group consisting of a defective allele, a homologue thereof, a fragment thereof, and a mixture thereof.

16. (Original) An animal of claim 15, wherein said defective allele is selected from the group consisting of defective alleles of RB genes, breast cancer suppressing genes, Wilm's tumor suppressing genes, Beckwith-Wiedemann syndrome suppressing genes, bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes, small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes, acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, homologues thereof, fragments thereof, and mixtures thereof.

17. (Original) An animal of claim 15, wherein said allele contains a DNA fragment having at least one defective nucleotide sequence.

18. (Original) An animal of claim 15, wherein said defective allele contains a DNA fragment having at least one defective RB nucleotide sequence.

19. (Original) The animal of claim 15, wherein said animal is a mouse.

20. (Original) A method for determining the carcinogenicity of suspected environmental influences, using the animal of claim 14, comprising the steps of:
 exposing said animal to a suspected environmental influence;
 observing the animal for the phenotypic expression of cancer; and
 determining carcinogenicity of the suspected environmental influence in response to observing a phenotypic expression of cancer in the animal.

21. (Original) A method of claim 20, wherein said exposing includes exposing to a source of radiation.

22. (Original) A method of claim 20, wherein said exposing includes exposing to tobacco combustion products.

23. (Original) A method of claim 20, wherein said exposing includes exposing to food additives.

24. (Original) A method of claim 20, wherein said exposing includes exposing to artificial substances.

25. (Original) A method of claim 20, wherein said observing includes examining the animal for tumor development.

26. (Original) A method of claim 25, wherein in response to the formation of a tumor in the animal, analyzing the tumor for the presence of cancer cells.

27. (Original) A method of making the animal of claim 15, comprising:
using at least one allele of an animal cancer suppressing gene selected from the group consisting of a defective allele, a homologue thereof, a fragment thereof, and a mixture thereof;

mutating at least one animal cell with said allele to form a mutated cell;

introducing said mutated cell into an animal blastocyst;

permitting growth of the blastocyst for a given period of time sufficient to incorporate said allele into its cells; repressing genetic recombinations within said cells; transferring the blastocyst containing said allele into the uterus of a pseudo pregnant animal for giving birth subsequently to an animal bearing said allele;

breeding said animal to reproduce additional animals; and

selecting the animal of claim 14 from said additional animals by determining the presence therein of the said allele.

28. (Original) A method of claim 27, wherein before introducing said allele, removing said blastocyst from a super ovulated animal, and wherein said blastocyst is comprised of undifferentiated cells.

29. (Original) A method of claim 27, wherein said introducing is performed in vitro.

30. (Original) A pharmaceutical composition wherein the active ingredient is selected from the group consisting of a naturally occurring intact cancer suppressing gene, a cloned intact cancer suppressing gene, fragments thereof, homologues thereof and mixtures thereof.

31. (Original) A pharmaceutical composition of claim 30, wherein said naturally occurring and cloned cancer suppressing gene is selected from the group consisting of RB genes, breast cancer suppressing genes, Wilm's tumor suppressing genes, Beckwith-Wiedemann syndrome suppressing genes, bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes, small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes, acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, homologues thereof, fragments thereof, and mixtures thereof.

32. (Original) A pharmaceutical composition of claim 30, wherein the active ingredient is selected from the group consisting of RB cDNA, modified RB cDNA fragment, clones thereof, homologues thereof and mixtures thereof.

33. (Original) A pharmaceutical composition of claim 31, wherein the active ingredient for each of said gene is selected from the group consisting of cDNA of said gene, fragments of said cDNA, homologues thereof and mixtures thereof.

34. (Original) A pharmaceutical composition of claim 32, wherein the cancer suppressing gene is isolated from human chromosome 13 region 13q14.

35. (Currently amended) A pharmaceutical composition of claim 31, wherein the cancer suppressing gene and its clone each has the following nucleotide sequence comprising SEQ ID NO:1:

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TTCCGGTTTT TCTCAGGGCA CGTTGAAATT ATTTTTGTAA CGGCAGTCCG CAGACCACCG      60
GGCGTGCCCC CGGTGCGCCC GCGTCGTCTT CCCCCGGCGCT CCTCCACAGC TCGCTGGCTC      120
CCGCCCCCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC      171
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
1 5 10
ACC GCC GCC GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC      219
Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
15 20 25
CCT CCG TAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTC CCT      267
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro
30 35 40
CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA      315
Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
45 50 55
TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC ACA GAG AGA GCT TGG      363
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
60 65 70 75
TTA ACT TGG GAG AAA GTT TCA TCT GTC GAT GGA GTA TTG GCA CGT TAT      411
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
80 85 90
ATT CAA AAG AAA AAG GAA CTG TCG GCA ATC TGT ATC TTT ATT GCA GCA      459
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
95 100 105
GTT GAC CTA CAT CAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC      507
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
110 115 120
ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT      555
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
125 130 135

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ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA ACA CTG TTC AAG AAG TAT 603
 Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
 140 145 150 155

GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGC ACA TGT GAA CTT 651
 Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
 160 165 170

ATA TAT TTG ACA CAA CCC AGC ACT TCG ATA TCT ACT CAA ATA AAT TCT 699
 Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser
 175 180 185

GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GCG 747
 Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly
 190 195 200

GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG 795
 Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met
 205 210 215

CTA TCT GTC CTT CAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC 843
 Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu
 220 225 230 235

AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA 891
 Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg
 240 245 250

ACA CCC ACC CGA GCT CAC AAC ACC AGT CCA CCG ATA GCA AAA CAA CTA 939
 Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu
 255 260 265

GAA AAT GAT ACA ACA ATT ATT CAA GTT CTC TGT AAA GAA CAT GAA TGT 987
 Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys
 270 275 280

AAT ATA CAT CAG GTC AAA AAT CTT TAT TTC AAA AAT TTT ATA CCT TTT 1035
 Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe
 285 290 295

ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA 1083
 Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu
 300 305 310 315

AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA 1131
 Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu
 320 325 330

GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT 1179
 Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser
 335 340 345

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ATA CAC ACT TTT GAA ACA CAG ACA ACA CCA CGA AAA ACT AAC CTT GAT	1227
Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp	
350 355 360	
GAA CAG GTC AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATC	1275
Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met	
365 370 375	
AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA ACT CAT CAA	1323
Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln	
380 385 390 395	
CCT TCA CAA AAT CTC ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA	1371
Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro	
400 405 410	
AAA CAA AGT ATA CTG AAA ACA GTG AAG CAT ATA GGA TAC ATC TTT AAA	1419
Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys	
415 420 425	
GAG AAA TTT GCT AAA GCT CTG CGA CAG GCT TGT CTC GAA ATT CGA TCA	1467
Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser	
430 435 440	
CAG CGA TAC AAA CTT GCA CTT CGC TTG TAT TAC CGA GTA ATG GAA TCC	1515
Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser	
445 450 455	
ATG CTT AAA TCA GAA CAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA	1563
Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys	
460 465 470 475	
CTT CTG AAT CAC AAC ATT TTT CAT ATG TCT TTA TTC GCG TGC CTT CTT	1611
Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu	
480 485 490	
GAG CTT GTA ATG GCC ACA TAT AGC ACA AGT ACA TCT CAG AAT CTT GAT	1659
Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp	
495 500 505	
TCT GCA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA	1707
Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu	
510 515 520	
AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA CAA	1755
Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu	
525 530 535	
GCC AAC TTG ACA ACA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT	1803
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His	
540 545 550 555	

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CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT 1851
 Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp
 560 565 570

CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA 1899
 Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu
 575 580 585

TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA 1947
 Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala
 590 595 600

GAT ATC TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT 1995
 Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr
 605 610 615

ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC 2043
 Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala
 620 625 630 635

TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT 2091
 Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr
 640 645 650

AAA AAA CTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA 2139
 Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu
 655 660 665

CGC CTT CTG TCT GAG CAC CCA CAA TTA CAA CAT ATC ATC TGG ACC CTT 2187
 Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu
 670 675 680

TTC CAG CAC ACC CTG CAG AAT CAG TAT GAA CTC ATG AGA GAG AGG CAT 2235
 Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His
 685 690 695

TTC CAC CAA ATT ATG ATG TCT TCC ATC TAT GCC ATA TGC AAA GTG AAG 2283
 Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys
 700 705 710 715

AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT 2331
 Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu
 720 725 730

CCT CAT GCT GTT CAG CAG ACA TTC AAA CGT GTT TTC ATC AAA CAA CAG 2379
 Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu
 735 740 745

GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATC CAG ACA 2427
 Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg
 750 755 760

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~~CTG AAA ACA AAT ATT TTG CAG TAT CCT TCC ACC AGG CCC CCT ACC TTG~~ 2475
~~Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu~~
~~765 770 775~~

~~TCA CCA ATA CCT CAC ATT CCT CCA AGC CCT TAC AAG TTT CCT AGT TCA~~ 2523
~~Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser~~
~~780 785 790 795~~

~~CCC TTA CGG ATT CCT GGA GCG AAC ATC TAT ATT TCA CCC CTC AAG AGT~~ 2571
~~Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser~~
~~800 805 810~~

~~CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA~~ 2619
~~Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro~~
~~815 820 825~~

~~AGA TCA AGA ATC TTA GTA TCA ATT CCT GAA TCA TTC GCG ACT TCT CAG~~ 2667
~~Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu~~
~~830 835 840~~

~~AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC~~ 2715
~~Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu~~
~~845 850 855~~

~~AAA ACA AGT GCT CAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA~~ 2763
~~Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu~~
~~860 865 870 875~~

~~CCC TTT GAT ATT GAA CCA TCA CAT GAA CCA GAT CCA AGT AAA CAT CTC~~ 2811
~~Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu~~
~~880 885 890~~

~~CCA GGA CAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT~~ 2859
~~Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr~~
~~895 900 905~~

~~CGA ACA CCA ATG CAA AAC CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA~~ 2907
~~Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser~~
~~910 915 920~~

~~AAC AAG GAA CAG AAA TGAGGATCTC AGGACCTTCG TGCACACTGT GTACACCTCT~~ 2962
~~Asn Lys Glu Glu Lys~~
~~925~~

~~GGATTCATTG TCTCTCACAG ATGTCACACTGT AT~~ 2994

36. (Original) A pharmaceutical composition of claim 32, wherein said RB cDNA fragment is selected from the group consisting of RB-1, RB-2, RB-5, y79R8 and mixtures thereof.

37. (Original) A pharmaceutical composition of claim 32, wherein a resulting mRNA transcript of said RB cDNA fragment has 4.6 kb.

38. (Original) A pharmaceutical composition of claim 37, wherein the cloned genomic DNA has at least 27 exons.

39. (Currently amended) A pharmaceutical composition of claim 30, wherein the cloned RB cDNA transcribes into mRNA which translates in protein having an amino acid sequence comprising SEQ ID NO:2:

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_____MPPKTPRKTAATAAAAAAEPAPPPPPPPPEEDPE_____ ( 34 )
QDSCPEDLPLVRLEFEETEEDFTALCQKLKIPDHVRERA_____ ( 74 )
WLTWEKVSSVDGVLGGYIQKKKELWGCICIFIAAVDLDEM_____ (114 )
FTFTELQKNIEISVHKFFNLLKEIDTSTKVDNAMSRLKK_____ (154 )
YDVLFALEFSKLERTCELIYLTQPSSSISTEINSALVLKVS_____ (194 )
WITFLLAKGEVLQMEDDLVISFQNLNLCVLDYFIKLSPPML_____ (234 )
LKEPYKTAVIPINGSPRTPRRRCQMRSAIAKQLENDTRII_____ (274 )
EVLCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEV_____ (314 )
ENLSKRYEEIYLLKNKDLARLFLDHDKTLOTDSDSIDSFETO_____ (354 )
RTPRKSNLDEEVNVIPPHHTPVRTVMNTIQQLMMLILNSASD_____ (394 )
QPSENLI SYFNNCTVNPKESILKRVKDICYIFKEKFAKAV_____ (434 )
GQGCVEIGSQRYKLGVRLYYRVME SMLKSEEEERLSIQNFS_____ (474 )
KLLNDNIFHMSLLACALEVVMATYSRSTSQNLDSCDTDL SF_____ (514 )
PWILNVLNLKAFDFYKVI ESFIKAECNL TREMIKHLERCE_____ (554 )
HRIMESLAWLSDSPLFDLIKQSKDREGPTDHLESACPLNL_____ (594 )
PLQNNHTAADMYLSPVRSPKKKGSTTRVNSTANAETQATS_____ (634 )
AFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHP_____ (674 )
ELEHIIWTLFQHTLQNEYELMRDRHLDQIMMCSMYGICKV_____ (714 )
KNIDLKFKIIVTAYKDLPHAVQETFKRVLIKEEYDSIIV_____ (754 )
FYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPS_____ (794 )
SPLRIPCGNIYISPLKSPYKISECLPTPTKMTPRSRI LVS_____ (834 )
IGESFGTSEKFQKINQMV CNSDRVLKRSAEGSNPPKPLKK_____ (874 )
LRFDIEGSD EADGSKHLPGESKFQQKLAEMTSTRTRMQKQ_____ (914 )
KMND SMDTSNKEEK_____ (928 )

```

~~single letter abbreviations for the amino acid residues are:~~
~~A, Ala; C, Cys; D, Asp; E, Gly; F, Phe; G, Gly; H, His;~~

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~~I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln;
 R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.~~

40. (Currently amended) A DNA nucleotide sequence comprising SEQ

ID NO:1:

```

TTCGCGTTTT TCTCAGGGGA CGTTGAAATT ATTTTTGTAA CCGGAGTCCG GAGAGCACCG ----- 60
GGCGTCCCCC GCGTGGCGGC GCGTGGTCCT CCGCGGCGCT CCTCCACAGC TCGCTGGCTC ----- 120
CCGCGCGCGA AAGGCGTC ATG CCG CCC AAA ACC CCG CGA AAA ACG GCC GCC ----- 171
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
1 5 10
ACC GCC GCC GCT GCC GCC GCG GAA CCG CCG GCA CCG CCG CCG CCG ----- 219
Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro
15 20 25
CCT CCG TAG CAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT ----- 267
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro
30 35 40
CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA ----- 315
Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
45 50 55
TTA TGT CAG AAA TTA AAG ATA CCA CAT CAT GTC AGA GAG AGA CCT TGG ----- 363
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
60 65 70 75
TTA ACT TCG CAG AAA GTT TCA TCT CTG GAT GCA GTA TTG CGA GGT TAT ----- 411
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
80 85 90
ATT CAA AAG AAA AAG GAA CTG TGG CGA ATC TGT ATC TTT ATT GCA GCA ----- 459
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
95 100 105
GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ----- 507
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
110 115 120
ATA GAA ATC ACT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT CAT ----- 555
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
125 130 135

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ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT 603
 Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
 140 145 150 155

GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT 651
 Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
 160 165 170

ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT 699
 Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser
 175 180 185

GCA TTG CTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GCG 747
 Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly
 190 195 200

GAA GTA TTA CAA ATG GAA GAT GAT CTG CTG ATT TCA TTT CAG TTA ATG 795
 Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met
 205 210 215

CTA TGT CTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC 843
 Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu
 220 225 230 235

AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA 891
 Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg
 240 245 250

ACA CCC AGG CGA GGT CAG AAC AGC AGT GCA CCG ATA GCA AAA CAA CTA 939
 Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu
 255 260 265

GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT 987
 Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys
 270 275 280

AAT ATA GAT GAG CTG AAA AAT CTT TAT TTC AAA AAT TTT ATA CCT TTT 1035
 Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe
 285 290 295

ATG AAT TCT CTT GCA CTT GTA ACA TCT AAT GCA CTT CCA GAG GTT GAA 1083
 Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu
 300 305 310 315

AAT CTT TCT AAA CGA TAC GAA CAA ATT TAT CTT AAA AAT AAA CAT CTA 1131
 Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu
 320 325 330

GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT 1179
 Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser
 335 340 345

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~~ATA CAC AGT TTT GAA ACA CAG ACA ACA CCA CGA AAA AGT AAC CTT GAT~~ 1227
~~Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp~~
~~350 355 360~~

~~GAA CAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG~~ 1275
~~Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met~~
~~365 370 375~~

~~AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA~~ 1323
~~Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln~~
~~380 385 390 395~~

~~CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA~~ 1371
~~Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro~~
~~400 405 410~~

~~AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA CGA TAC ATC TTT AAA~~ 1419
~~Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys~~
~~415 420 425~~

~~GAG AAA TTT CCT AAA CCT CTG CGA CAG GGT TGT GTC GAA ATT CGA TCA~~ 1467
~~Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser~~
~~430 435 440~~

~~CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC~~ 1515
~~Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser~~
~~445 450 455~~

~~ATG CTT AAA TCA CAA CAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA~~ 1563
~~Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys~~
~~460 465 470 475~~

~~CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT~~ 1611
~~Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu~~
~~480 485 490~~

~~GAG GTT GTA ATG GCC ACA TAT AGC ACA AGT ACA TCT CAG AAT CTT GAT~~ 1659
~~Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp~~
~~495 500 505~~

~~TCT CGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTC CTT AAT TTA~~ 1707
~~Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu~~
~~510 515 520~~

~~AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA CCA GAA~~ 1755
~~Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu~~
~~525 530 535~~

~~GCC AAC TTC ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT~~ 1803
~~Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His~~
~~540 545 550 555~~

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CGA ATC ATG GAA TCC CTT GCA TCG CTC TCA GAT TCA CCT TTA TTT GAT 1851
 Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp
 560 565 570

CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA 1899
 Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu
 575 580 585

TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA 1947
 Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala
 590 595 600

GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT 1995
 Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr
 605 610 615

ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC 2043
 Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala
 620 625 630 635

TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT 2091
 Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr
 640 645 650

AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA 2139
 Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu
 655 660 665

CGC CTT CTC TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT 2187
 Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu
 670 675 680

TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT 2235
 Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His
 685 690 695

TTC CAC CAA ATT ATG ATG TCT TCC ATG TAT GCC ATA TGC AAA CTG AAG 2283
 Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys
 700 705 710 715

AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT 2331
 Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu
 720 725 730

CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT CTT TTC ATC AAA GAA CAG 2379
 Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu
 735 740 745

GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG CTC TTC ATC CAG AGA 2427
 Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg
 750 755 760

~~CTG AAA ACA AAT ATT TTC CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG~~ 2475
~~Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu~~
~~765 770 775~~

~~TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT ACT TCA~~ 2523
~~Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser~~
~~780 785 790 795~~

~~CCC TTA CGG ATT CCT GCA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT~~ 2571
~~Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser~~
~~800 805 810~~

~~CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA~~ 2619
~~Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro~~
~~815 820 825~~

~~AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG~~ 2667
~~Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu~~
~~830 835 840~~

~~AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC~~ 2715
~~Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu~~
~~845 850 855~~

~~AAA ACA AGT CCT CAA GCA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA~~ 2763
~~Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu~~
~~860 865 870 875~~

~~CCC TTT GAT ATT CAA GCA TCA GAT CAA GCA CAT CCA AGT AAA CAT CTC~~ 2811
~~Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu~~
~~880 885 890~~

~~CCA GCA GAG TCC AAA TTT CAG CAG AAA CTG CCA GAA ATG ACT TCT ACT~~ 2859
~~Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr~~
~~895 900 905~~

~~CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT ACC ATG CAT ACC TCA~~ 2907
~~Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser~~
~~910 915 920~~

~~AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTCG TGGACACTCT GTACACCTCT~~ 2962
~~Asn Lys Glu Glu Lys~~
~~925~~

~~GGATTCATTG TCTCTCACAG ATGTCACTGT AT~~ 2994

41. (Original) A method of therapeutically treating inactive, mutative or absent cancer suppressing genes comprising:

treating said inactive, mutative or absent cancer suppressing genes with at least a portion of intact cancer suppressing genes.

42. (Original) A method of claim 41, wherein said cancer suppressing genes are each a substance selected from the groups consisting of RB genes, breast cancer suppressing genes, Wilm's tumor suppressing genes, Beckwith-Wiedemann syndrome suppressing genes, bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes, small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes, acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, and mixtures thereof.

43. (Original) A method of claim 41, wherein said treating includes: treating said inactive, mutative or absent cancer suppressing gene with a substance selected from the group consisting of an RB gene, a portion of said gene, or a mixture thereof.

44. (Original) A method of claim 43, wherein said portion is selected from the group consisting of RB cDNA, RB cDNA fragment, homologues thereof and mixtures thereof.

45. (Original) The method of claim 41, wherein the intact cancer suppressing gene, or portion thereof, is delivered to the site of a tumor by means of a retrovirus.

46. (Original) A method of claim 41, wherein the intact cancer suppressing gene, or a portion thereof, is delivered to the site of a tumor by a liposome.

47. (Original) A method of claim 41, wherein the location of said cancer suppressing gene is determined by utilizing a genetic marker.